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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/068,956
DATE: 03/19/2002
TIME: 17:50:38

Input Set : N:\Crf3\02272002\J068956.raw
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1 <110> APPLICANT: Paul Young et al.
2 <120> TITLE OF INVENTION: PGRP-L Polynucleotides, Polypeptides, and Antibodies
3 <130> FILE REFERENCE: PF513P1
4 <140> CURRENT APPLICATION NUMBER: US/10/068,956
5 <141> CURRENT FILING DATE: 2002-02-11
6 <150> PRIOR APPLICATION NUMBER: 60/149,715
7 <151> PRIOR FILING DATE: 1999-08-20
8 <150> PRIOR APPLICATION NUMBER: PCT/US00/22877
9 <151> PRIOR FILING DATE: 2000-08-18
10 <160> NUMBER OF SEQ ID NOS: 18
11 <170> SOFTWARE: PatentIn version 3.1
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15 <212> TYPE: DNA
16 <213> ORGANISM: human
17 <400> SEQUENCE: 1
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20   gcgacacgct cccgagttgt gcggtgcgcg ccggcctcct gcggccagac tacgcgctgc      180
21   tggggccaccg ccagctggtg cgcaccgact gcccggcgca cgcgctcttc gacctgctgc      240
22   gcaactggcc gcacttcacc gcggtgagtc ttgcagcct gcactacacg gcccgccgcc      300
23   cctccgtcta cacaagctcc acgaggcccc tgcccctgc ctgtaacagc tgtgcccgca      360
24   cagcctcagc caggcccca acttcccggc ggcacgtcta ttcaggaaac ctaggccag      420
25   cctttgcggg tcaactctgc ggcaacatcc ctgatcctgt gacttctgcc tatgcagcct      480
26   cagctcagcc ccagaccag ccagcctgtc ctttcccag ctctaatac ctctaccttt      540
27   ccagccaagg catggaccct gacacctgcc aacagcccct ctgccctcac aacctcagcc      600
28   tggccttcat gacttctcta cccaagtcac aacctgtcag gctgcaccac ctcatcctgg      660
29   cccgcgaac cttgacctca cccctgcccc taccogaagg ctctctgtcc acacaacatg      720
30   aacctagget gtgacctttt gccttcacaa cctctgtcca gtocctaatc ctgtgttgca      780
31   attctctgtc cagacaatct caactctgag gttgcttgtt tcgtccctga ctccctaacc      840
32   cctgatgaca actcttatgc cagcacaact ttgacctgat gacctcatcc cagcccttga      900
33   tcgccatcac taaaacaatt ttagaatcac acctggacaa tctcgtgcta cctacatact      960
34   gccactccat ttcattaagc tattgactag cacatccatc tcggcctata gttggctttg     1020
35   tcctcaactc ctcaacttgg gccactgtcc cctccctgat aaaggggata tcaccaccga     1080
36   tcccacagaa atacaaacta ccatcagaga atactataaa caoctctatg caaataaact     1140
37   agaaaatcta gaagaaatgg ataaattcct caacaccac taccaaaaaa aaaaaaaaaa     1200
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40 <211> LENGTH: 174
41 <212> TYPE: PRT
42 <213> ORGANISM: human
43 <400> SEQUENCE: 2
44   Arg Gly Trp His Trp Val Gly Ala His Thr Leu Gly His Asn Ser Arg
45   1                               5                               10                               15
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46 Gly Phe Gly Val Ala Ile Val Gly Asn Tyr Thr Ala Ala Leu Pro Thr
47 20 25 30
48 Glu Ala Ala Leu Arg Thr Val Arg Asp Thr Leu Pro Ser Cys Ala Val
49 35 40 45
50 Arg Ala Gly Leu Leu Arg Pro Asp Tyr Ala Leu Leu Gly His Arg Gln
51 50 55 60
52 Leu Val Arg Thr Asp Cys Pro Gly Asp Ala Leu Phe Asp Leu Leu Arg
53 65 70 75 80
54 Thr Trp Pro His Phe Thr Ala Val Ser Leu Arg Ser Leu His Tyr Thr
55 85 90 95
56 Ala Arg Arg Pro Ser Val Tyr Thr Ser Ser Thr Arg Pro Leu Pro Pro
57 100 105 110
58 Ala Cys Asn Ser Cys Ala Arg Thr Ala Ser Ala Arg Pro Pro Thr Ser
59 115 120 125
60 Arg Arg His Val Tyr Ser Gly Asn Leu Gly Pro Ala Phe Ala Gly His
61 130 135 140
62 Ser Ala Gly Asn Ile Pro Asp Pro Val Thr Ser Ala Tyr Ala Ala Ser
63 145 150 155 160
64 Ala Gln Pro Gln Thr Gln Pro Ala Cys Pro Phe Pro Ser Ser
65 165 170

67 <210> SEQ ID NO: 3

68 <211> LENGTH: 1876

69 <212> TYPE: DNA

70 <213> ORGANISM: human

71 <400> SEQUENCE: 3

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74 tctgtcgggt ctgtgccctg gaactggaga cccaccatga aggcctgggg tgccctctgg 180
75 atcgtgcttg gattgctgct gtggccagag ccaggggcag cctcctcctt gcctctgctc 240
76 atggactcca tcatccaggc ccttgctgaa cttgagcaaa aggtaccagt gactgaggcc 300
77 agcatcactg cctctgcatg gattctgtca gccagaact ccagcaccga caattccctt 360
78 caccagcgtc tgctgctgaa ggcaccaagc cacaacacta cagagccaga tctcactct 420
79 ctacgcccgg agcttcaagc actgatttct gaggtggctc aacacgatgt acagaatggg 480
80 cggaatatg gagtggtgct ggcacctgat ggctccaccg tagctgtgaa gcctctgctg 540
81 tttgggctag aggcgggtct acaggcacac agcgttgcta acttgccctc agattgtctg 600
82 gctatcccct gtgatactgg agacaccttg gccaatatta gagccacctg gccaggactc 660
83 atggatgctt ttccaaatgc ctcttctoca gatgttgag ccactttacc aaacgacaaa 720
84 gccaaagatc ccaccactgt ggacagactc ctggcaatca ccttggctgg tgacttaggt 780
85 ctgaccttcc tccacaggtc ccagacttgg agtccctcag gactgggaac tgagggtgctc 840
86 tgggaccagc ttactgcccc cagggtcttc aactgttgga acccccaggc atccaggctc 900
87 accatggctt tctcaatgg tgcttagat ggagctctcc ttgggaacca cttgagccaa 960
88 atccctaggc cccaccacc cctcagccac ctgctaagag agtactatgg agctgggggtg 1020
89 aatggagatc cgggtgttccg aagtaacttc cgaaggcaga acggtgctgc tttgacttca 1080
90 gccctacccc tggcccagca ggtatgggag gcccttgctc tgttacagaa actggagcca 1140
91 gaacacctac agttgcagaa cattagccaa gagcagctgg ctacaggtagc caccttggct 1200
92 accaaggagt tcaactgaggc ttctctggga tgcccagcca ttcacccccg ctgccgttgg 1260
93 ggagcggctc cctaccgagg ccacccaaca ccactccggc tgccacttgg attcttatat 1320
94 gtgcatacaca catacgtgcc agcgccaccc tgcaccacct tccagagctg cgccgcgat 1380
95 atgcgtcca tgcagcgttt ccaccaggat gtgcgcaagt gggatgacat cggttacagt 1440

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97      cacacacgcg gctacaactc ccgcggcttc ggtgtggcct tcgtgggcaa ctacactggg 1560
98      tcactgcca acgaagctgc gctgaacacg gtgcgcgacg cgctcccgag ctgcgcaatt 1620
99      cgccaaggtc tcttgcgggc agactacaag ctgcttgccc accgccagct agtgctcacc 1680
100     cactgccccg ggaacgcgct cttcaacttg ctgcgcacct ggcctcactt cacagagggt 1740
101     gaaaactaag aactcctttg agagaccctt gaagatccag gaggtattat ccctgatgat 1800
102     cctttgagca accacagacc tccaataaag ggaccactga aaggaaaaaa aaaaaaaaaa 1860
103     aaaaaaaaaa aaaaaa 1876
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106 <211> LENGTH: 530
107 <212> TYPE: PRT
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109 <400> SEQUENCE: 4
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113     20 25 30
114     Ile Gln Ala Leu Ala Glu Leu Glu Gln Lys Val Pro Val Thr Glu Ala
115     35 40 45
116     Ser Ile Thr Ala Ser Ala Trp Ile Leu Ser Ala Lys Asn Ser Ser Thr
117     50 55 60
118     His Asn Ser Leu His Gln Arg Leu Leu Leu Lys Ala Pro Ser His Asn
119     65 70 75 80
120     Thr Thr Glu Pro Asp Pro His Ser Leu Ser Pro Glu Leu Gln Ala Leu
121     85 90 95
122     Ile Ser Glu Val Ala Gln His Asp Val Gln Asn Gly Arg Glu Tyr Gly
123     100 105 110
124     Val Val Leu Ala Pro Asp Gly Ser Thr Val Ala Val Lys Pro Leu Leu
125     115 120 125
126     Phe Gly Leu Glu Ala Gly Leu Gln Ala His Ser Val Ala Asn Leu Pro
127     130 135 140
128     Ser Asp Cys Leu Ala Ile Pro Cys Asp Thr Gly Asp Thr Leu Ala Asn
129     145 150 155 160
130     Ile Arg Ala Thr Trp Pro Gly Leu Met Asp Ala Phe Pro Asn Ala Ser
131     165 170 175
132     Ser Pro Asp Val Gly Ala Thr Leu Pro Asn Asp Lys Ala Lys Thr Pro
133     180 185 190
134     Thr Thr Val Asp Arg Leu Leu Ala Ile Thr Leu Ala Gly Asp Leu Gly
135     195 200 205
136     Leu Thr Phe Leu His Arg Ser Gln Thr Trp Ser Pro Pro Gly Leu Gly
137     210 215 220
138     Thr Glu Gly Cys Trp Asp Gln Leu Thr Ala Pro Arg Val Phe Thr Leu
139     225 230 235 240
140     Leu Asp Pro Gln Ala Ser Arg Leu Thr Met Ala Phe Leu Asn Gly Ala
141     245 250 255
142     Leu Asp Gly Ala Leu Leu Gly Asn His Leu Ser Gln Ile Pro Arg Pro
143     260 265 270
144     His Pro Pro Leu Ser His Leu Leu Arg Glu Tyr Tyr Gly Ala Gly Val
145     275 280 285
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146	Asn Gly Asp Pro Val Phe Arg Ser Asn Phe Arg Arg Gln Asn Gly Ala	
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148	Ala Leu Thr Ser Ala Pro Thr Leu Ala Gln Gln Val Trp Glu Ala Leu	
149	305 310 315 320	
150	Val Leu Leu Gln Lys Leu Glu Pro Glu His Leu Gln Leu Gln Asn Ile	
151	325 330 335	
152	Ser Gln Glu Gln Leu Ala Gln Val Ala Thr Leu Ala Thr Lys Glu Phe	
153	340 345 350	
154	Thr Glu Ala Phe Leu Gly Cys Pro Ala Ile His Pro Arg Cys Arg Trp	
155	355 360 365	
156	Gly Ala Ala Pro Tyr Arg Gly His Pro Thr Pro Leu Arg Leu Pro Leu	
157	370 375 380	
158	Gly Phe Leu Tyr Val His His Thr Tyr Val Pro Ala Pro Pro Cys Thr	
159	385 390 395 400	
160	Thr Phe Gln Ser Cys Ala Ala Asp Met Arg Ser Met Gln Arg Phe His	
161	405 410 415	
162	Gln Asp Val Arg Lys Trp Asp Asp Ile Gly Tyr Ser Phe Val Val Gly	
163	420 425 430	
164	Ser Asp Gly Tyr Leu Tyr Gln Gly Arg Gly Trp His Trp Val Gly Ala	
165	435 440 445	
166	His Thr Arg Gly Tyr Asn Ser Arg Gly Phe Gly Val Ala Phe Val Gly	
167	450 455 460	
168	Asn Tyr Thr Gly Ser Leu Pro Asn Glu Ala Ala Leu Asn Thr Val Arg	
169	465 470 475 480	
170	Asp Ala Leu Pro Ser Cys Ala Ile Arg Glu Gly Leu Leu Arg Pro Asp	
171	485 490 495	
172	Tyr Lys Leu Leu Gly His Arg Gln Leu Val Leu Thr His Cys Pro Gly	
173	500 505 510	
174	Asn Ala Leu Phe Asn Leu Leu Arg Thr Trp Pro His Phe Thr Glu Val	
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176	Glu Asn	
177	530	
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182	<213> ORGANISM: human	
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186	tctcccgagc tctgaggtc acatgcgtgg tggtagcgtt aagccacgaa gacctgagg	180
187	tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg	240
188	aggagcagta caacagcacg tacctgtgtg tcagcgtcct caccgtcctg caccaggact	300
189	ggctgaatgg caaggagtac aagtgcgaagg tctccaacaa agccctccca accccatcg	360
190	agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc	420
191	catcccgagg tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct	480
192	atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga	540
193	ccacgcctcc cgtgctggac tccgacggct ccttcttctt ctacagcaag ctaccgtgg	600
194	acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggtctctg	660
195	acaaccacta cagcgagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc	720

Input Set : N:\Crf3\02272002\J068956.raw
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196 gactctagag gat 733
198 <210> SEQ ID NO: 6
199 <211> LENGTH: 5
200 <212> TYPE: PRT
201 <213> ORGANISM: human
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203 <221> NAME/KEY: MISC_FEATURE
204 <222> LOCATION: (3)..(3)
205 <223> OTHER INFORMATION: Xaa equals any amino acid
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207 Trp Ser Xaa Trp Ser
208 1 5
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211 <211> LENGTH: 86
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213 <213> ORGANISM: human
214 <400> SEQUENCE: 7
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216 cccgaaatat ctgccatctc aattag 86
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219 <211> LENGTH: 27
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221 <213> ORGANISM: human
222 <400> SEQUENCE: 8
223 gcggcaagct ttttgcaaag cctagggc 27
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228 <213> ORGANISM: human
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231 aaatatctgc catctcaatt agtcagcaac catagtcccc cccctaactc cgcccatccc 120
232 gccctaact ccgccagtt ccgccattc tccgccccat ggcctgactaa ttttttttat 180
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244 <211> LENGTH: 31
245 <212> TYPE: DNA
246 <213> ORGANISM: human
247 <400> SEQUENCE: 11
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